SEQUENCE LISTING

<110> Curtis, Rory A.J.
      Millennium Pharmaceuticals Inc.

<120> 25466, A Human Transporter and Uses
   Therefor

<130> MPI2001-019P1RCP1(M)

<150> 60/269072
<151> 2001-02-15

<160> 8

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 4419
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (449)...(1981)

<400> 1
gtcgacccac gcgtccgcaa gagtgtgcat gtgaggtgac tgcatttttt ttccctgcca 60
aaccagaatt agccggtata ggaatgaacg agcatgaaga tttgaaattg ctccgattgg 120
aaggaagccc aggttaggtt tgggcacctc caaacgcacc cgtttttaaag ccacctggac 180
tgaggcgtcg agctttcagc tccaccaaac gctcacctgg cctggcagcg agcggcggaa 240
gagcccggga gcccctcaca gagcgcaccg agccgggcgg agagctgagc cgcaggcacc 300
cgcgtctcca ggatgatagg cgacattgca acaaatctct acacccagca gctcaggggg 360
ctccaagcag agcagcaagt tcgaggatcc gggcgtggag ccgagtgagg ccgcagccca 420
gcgggcctcg ggcgaaaaat cttggaaa atg tat acc agt cat gaa gat att   472
                                 Met Tyr Thr Ser His Glu Asp Ile
                                  1   5

ggg tat gat ttt gaa gat ggc ccc aaa gac aaa aag aca ctg aag ccc   520
Gly Tyr Asp Phe Glu Asp Gly Pro Lys Asp Lys Lys Thr Leu Lys Pro
     10   15   20

cac cca aac att gat ggc gga tgg gct tgg atg atg gtg ctc tcc tct   568
His Pro Asn Ile Asp Gly Gly Trp Ala Trp Met Met Val Leu Ser Ser
 25   30   35   40

ttc ttt gtg cac atc ctc atc atg ggc tcc cag atg gcc ctg ggt gtc   616
Phe Phe Val His Ile Leu Ile Met Gly Ser Gln Met Ala Leu Gly Val
                 45   50   55

ctc aac gtg gaa tgg ctg gaa gaa ttc cac cag agc cgc ggc ctg acc   664
Leu Asn Val Glu Trp Leu Glu Glu Phe His Gln Ser Arg Gly Leu Thr
                 60   65   70

gcc tgg gtc agc tcc ctc agc atg ggc atc acc ttg ata gtg ggc cct   712
Ala Trp Val Ser Ser Leu Ser Met Gly Ile Thr Leu Ile Val Gly Pro
         75   80   85

ttc atc ggc ttg ttc att aac acc tgt ggg tgc cgc cag act gcg atc   760
Phe Ile Gly Leu Phe Ile Asn Thr Cys Gly Cys Arg Gln Thr Ala Ile

- 1 -

```
                    90                      95                      100
att gga ggg ctc gtc aac tcc ctg ggc tgg gtg ttg agt gcc tat gct    808
Ile Gly Gly Leu Val Asn Ser Leu Gly Trp Val Leu Ser Ala Tyr Ala
105                     110                     115                 120

gca aac gtg cat tat ctc ttc att act ttt gga gtc gca gct ggc ctg    856
Ala Asn Val His Tyr Leu Phe Ile Thr Phe Gly Val Ala Ala Gly Leu
                    125                     130                 135

ggc agc ggg atg gcc tac ctg cca gcg gtg gtc atg gtg ggc agg tat    904
Gly Ser Gly Met Ala Tyr Leu Pro Ala Val Val Met Val Gly Arg Tyr
                140                     145                 150

ttc cag aag aga cgc gcc ctc gcc cag ggc ctc agc acc acg ggg acc    952
Phe Gln Lys Arg Arg Ala Leu Ala Gln Gly Leu Ser Thr Thr Gly Thr
                155                     160                 165

gga ttc ggt acg ttc cta atg act gtg ctg ctg aag tac ctg tgc gca   1000
Gly Phe Gly Thr Phe Leu Met Thr Val Leu Leu Lys Tyr Leu Cys Ala
                170                     175                 180

gag tac ggc tgg agg aat gcc atg ttg atc caa ggt gcc gtt tcc cta   1048
Glu Tyr Gly Trp Arg Asn Ala Met Leu Ile Gln Gly Ala Val Ser Leu
185                     190                     195                 200

aac ctg tgt gtt tgt ggg gcg ctc atg agg ccc ctc tct cct ggt aaa   1096
Asn Leu Cys Val Cys Gly Ala Leu Met Arg Pro Leu Ser Pro Gly Lys
                    205                     210              215

aac cca aac gac cca gga gag aaa gat gtg cgt ggc ctg cca gcg cac   1144
Asn Pro Asn Asp Pro Gly Glu Lys Asp Val Arg Gly Leu Pro Ala His
                220                     225                 230

tcc aca gaa tct gtg aag tca act gga cag cag gga aga aca gaa gag   1192
Ser Thr Glu Ser Val Lys Ser Thr Gly Gln Gln Gly Arg Thr Glu Glu
                235                     240                 245

aag gat ggt ggg ctc ggg aac gag gag acc ctc tgc gac ctg caa gcc   1240
Lys Asp Gly Gly Leu Gly Asn Glu Glu Thr Leu Cys Asp Leu Gln Ala
                250                     255                 260

cag gag tgc ccc gat cag gcc ggg cac agg aag aac atg tgt gcc ctc   1288
Gln Glu Cys Pro Asp Gln Ala Gly His Arg Lys Asn Met Cys Ala Leu
265                     270                     275                 280

cgg att ctg aag act gtc agc tgg ctc acc atg aga gtc agg aag ggc   1336
Arg Ile Leu Lys Thr Val Ser Trp Leu Thr Met Arg Val Arg Lys Gly
                    285                     290                 295

ttc gag gac tgg tat tcg ggc tac ttt ggg aca gcc tct cta ttt aca   1384
Phe Glu Asp Trp Tyr Ser Gly Tyr Phe Gly Thr Ala Ser Leu Phe Thr
                300                     305                 310

aat cga atg ttt gta gcc ttt att ttc tgg gct ttg ttt gca tac agc   1432
Asn Arg Met Phe Val Ala Phe Ile Phe Trp Ala Leu Phe Ala Tyr Ser
                315                     320                 325

agc ttt gtc atc ccc ttc att cac ctc cca gaa atc gtc aat ttg tat   1480
Ser Phe Val Ile Pro Phe Ile His Leu Pro Glu Ile Val Asn Leu Tyr
                330                     335                 340
```

- 2 -

```
aac tta tcg gag caa aac gac gtt ttc cct ctg acg tca att ata gca   1528
Asn Leu Ser Glu Gln Asn Asp Val Phe Pro Leu Thr Ser Ile Ile Ala
345                 350             355                 360

ata gtt cac atc ttt gga aaa gtg atc ctg ggc gtc ata gcc gac ttg   1576
Ile Val His Ile Phe Gly Lys Val Ile Leu Gly Val Ile Ala Asp Leu
                365             370                 375

cct tgc att agt gtt tgg aat gtc ttc ctg ttg gcc aac ttc acc ctt   1624
Pro Cys Ile Ser Val Trp Asn Val Phe Leu Leu Ala Asn Phe Thr Leu
                380             385                 390

gtc ctc agt att ttt att ctg ccg ttg atg cac acg tac gct ggc ctg   1672
Val Leu Ser Ile Phe Ile Leu Pro Leu Met His Thr Tyr Ala Gly Leu
                395             400                 405

gcg gtc atc tgt gcg ctg ata ggg ttt tcc agt ggt tat ttc tcc cta   1720
Ala Val Ile Cys Ala Leu Ile Gly Phe Ser Ser Gly Tyr Phe Ser Leu
    410             415                 420

atg ccc gta gtg act gaa gac ttg gtt ggc att gaa cac ctg gcc aat   1768
Met Pro Val Val Thr Glu Asp Leu Val Gly Ile Glu His Leu Ala Asn
425                 430             435                 440

gcc tac ggc atc atc atc tgt gct aat ggc atc tct gca ttg ctg gga   1816
Ala Tyr Gly Ile Ile Ile Cys Ala Asn Gly Ile Ser Ala Leu Leu Gly
                445             450                 455

cca cct ttt gca ggg tgg atc tat gac atc acg caa aaa tat gat ttt   1864
Pro Pro Phe Ala Gly Trp Ile Tyr Asp Ile Thr Gln Lys Tyr Asp Phe
                460             465                 470

tcc ttc tac ata tgt ggt ttg ctt tac atg ata gga ata ctc ttt tta   1912
Ser Phe Tyr Ile Cys Gly Leu Leu Tyr Met Ile Gly Ile Leu Phe Leu
                475             480                 485

ctt att cag ccg tgc att cga att ata gaa caa tcc aga aga aaa tac   1960
Leu Ile Gln Pro Cys Ile Arg Ile Ile Glu Gln Ser Arg Arg Lys Tyr
    490             495                 500

atg gat ggt gca cat gtt tag tatcatgtaa tgttccgtgt aggtttcatt   2011
Met Asp Gly Ala His Val  *
505                 510

gtaatactca tgcctacctc gcatggttgc tgtgaggcac ctatgacagg acgtgggaaa 2071
gcattttgta cggtaactgg cactgtcatt tgtaaatgcc attgtcacag cctcatttgt 2131
aagcagcact gcctctctgt ttggggagat gtaatgctgg aagatcttaa ggactacata 2191
cattctagag atgacagtgt tgttcaaaga cagcctagta agtaattggt agaaatgccc 2251
ttataaaaac cattctcttg tcatctactg ggactagggt tttaaataca gcttttaaaa 2311
acaaaaacag ggaataaaag cttttcaact caaccacttc tttgtaagac aaaactgaag 2371
tatctgtgtg cttccagaaa gcttacagat aaatgggttt caagcacaag aatatgacta 2431
gatttcagaa attaattatt acagggagct attgatctac tagcatcaaa caaaggcaag 2491
ctctaattcc acaggtaata caatttagtg caattaaaga aacacggctt gtattttat  2551
gagggaattc tgcagctagg gattgtgact cctaaatcct cctctaaaag aaggcacttg 2611
ccattaatcc taattcagtg ctatccagtt ataaatggaa tcttgagaca aaaccttaac 2671
aaagaaataa cagtaatgat ttccttagca gaagccgtat ttgtacgcac aacattaaat 2731
caagggctac aattcaagca ctttttattcg tatcattggc ctcttagatg atataagcat 2791
gaggtggggc ctgtaatatt tttttctgag tttcttctgc ccaaaaatat aatatagaac 2851
taattgctaa ctgacaaata aagttaatag ttaaatcatc tccaaggaat gttgctaatc 2911
caaagtataa cactatcaat ttgtgaggat aataaatgga atgccattag tgtagatgtc 2971
```

- 3 -

```
tgtgccacat ctgacactgg agtagtgata acaaatagcc catctctaga ctctcgtgtt 3031
gttatataga ccattcattt gcctgagcgt ggcacagttt taaaaatagt tctcttgatt 3091
gatttcatac agaagatgac tgtgatccat gacatctaat aatgcccttt ctttatctga 3151
gatgtctatt tttctaagcc aaacgttttt cagactgcag aatgttcttc ccagatcatt 3211
tgaaatttct ggctgcctta cttgtttaca gatagtttaa gactatttaa atttctactc 3271
acaatttgat catcacacac acacaaatcc ttgaatatca ttgccagtgt cttaggtcaa 3331
atttacctaa agtgaataca gcccattctc aattatcctt cacaattaga cgcaggaatg 3391
ctactaggaa ttggaatcaa acaatgccac cccaagcgta attttagcca gcagtttcag 3451
ttatactcaa ccatgtcctt ctgagctgtt aacaagtgat tcaatggaca agttctcttt 3511
ttgttccatc tccattattt cctgctctaa tgtatagtgg gagtggttgt gtaatgaaag 3571
gaccaccaaa ataataaaag gcagctaatg gaaaggagag acaaaagcat ggttaatata 3631
tatacttaat attacctcca atgactcggg aattgcctgt aaattattat agacaataga 3691
ttgcatgtca tactccattt ggttcaacac aacaacctat gtgttatcat tacagctttg 3751
gctgctgtta aagaatccag ctctctattt tgataaagat aatcttaaag ctgaggcaat 3811
gctccctccc ctatctctct ctgtgtaatt taccatagaa ttaggatgat tagattgaaa 3871
cacatgttgt atgttttaaa aactacattg cttcattact ttcattttcc gacaacatca 3931
aactaacaag aggcagtgtt aaatatttta aatggtgcta tagccaatgt atttgaatgc 3991
ttgcactgct ggttgtgtat catcaatatg aacttttat ccaatgactc aactctaatt 4051
acatctaagt tagacttgct cacgttcagt ttgtacagtt gtgtgttgac ttactatgtt 4111
ttgaaagtgg tgacttctac cgaatgagtg gaagttccca ttgtcaaaaa aaataaagac 4171
ctgcttgcag tattcatgtt gacaacagag taaaagagaa tactgtaaag aattactgca 4231
aatatttcct gtttatgtta tttgccgttg tttgaagata ttataaaggg ttaattgtat 4291
atttatatca tgtgctttat cgttttcccc tcatgtatcc aagtaatttt tatttacata 4351
caactaaata aatgttgtcc tctttgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaagggg 4411
gcggccgc                                                           4419
```

<210> 2
<211> 510
<212> PRT
<213> homo sapiens

<400> 2
```
Met Tyr Thr Ser His Glu Asp Ile Gly Tyr Asp Phe Glu Asp Gly Pro
  1               5                  10                  15
Lys Asp Lys Lys Thr Leu Lys Pro His Pro Asn Ile Asp Gly Gly Trp
             20                  25                  30
Ala Trp Met Met Val Leu Ser Ser Phe Phe Val His Ile Leu Ile Met
         35                  40                  45
Gly Ser Gln Met Ala Leu Gly Val Leu Asn Val Glu Trp Leu Glu Glu
     50                  55                  60
Phe His Gln Ser Arg Gly Leu Thr Ala Trp Val Ser Ser Leu Ser Met
65                  70                  75                  80
Gly Ile Thr Leu Ile Val Gly Pro Phe Ile Gly Leu Phe Ile Asn Thr
                 85                  90                  95
Cys Gly Cys Arg Gln Thr Ala Ile Ile Gly Gly Leu Val Asn Ser Leu
            100                 105                 110
Gly Trp Val Leu Ser Ala Tyr Ala Ala Asn Val His Tyr Leu Phe Ile
        115                 120                 125
Thr Phe Gly Val Ala Ala Gly Leu Gly Ser Gly Met Ala Tyr Leu Pro
    130                 135                 140
Ala Val Val Met Val Gly Arg Tyr Phe Gln Lys Arg Arg Ala Leu Ala
145                 150                 155                 160
Gln Gly Leu Ser Thr Thr Gly Thr Gly Phe Gly Thr Phe Leu Met Thr
                165                 170                 175
Val Leu Leu Lys Tyr Leu Cys Ala Glu Tyr Gly Trp Arg Asn Ala Met
            180                 185                 190
Leu Ile Gln Gly Ala Val Ser Leu Asn Leu Cys Val Cys Gly Ala Leu
        195                 200                 205
Met Arg Pro Leu Ser Pro Gly Lys Asn Pro Asn Asp Pro Gly Glu Lys
    210                 215                 220
Asp Val Arg Gly Leu Pro Ala His Ser Thr Glu Ser Val Lys Ser Thr
```

- 4 -

```
     225                     230                     235                     240
Gly Gln Gln Gly Arg Thr Glu Glu Lys Asp Gly Gly Leu Gly Asn Glu
                     245                     250                     255
Glu Thr Leu Cys Asp Leu Gln Ala Gln Glu Cys Pro Asp Gln Ala Gly
             260                     265                     270
His Arg Lys Asn Met Cys Ala Leu Arg Ile Leu Lys Thr Val Ser Trp
             275                     280                     285
Leu Thr Met Arg Val Arg Lys Gly Phe Glu Asp Trp Tyr Ser Gly Tyr
     290                     295                     300
Phe Gly Thr Ala Ser Leu Phe Thr Asn Arg Met Phe Val Ala Phe Ile
305                     310                     315                     320
Phe Trp Ala Leu Phe Ala Tyr Ser Ser Phe Val Ile Pro Phe Ile His
                 325                     330                     335
Leu Pro Glu Ile Val Asn Leu Tyr Asn Leu Ser Glu Gln Asn Asp Val
             340                     345                     350
Phe Pro Leu Thr Ser Ile Ile Ala Ile Val His Ile Phe Gly Lys Val
             355                     360                     365
Ile Leu Gly Val Ile Ala Asp Leu Pro Cys Ile Ser Val Trp Asn Val
     370                     375                     380
Phe Leu Leu Ala Asn Phe Thr Leu Val Leu Ser Ile Phe Ile Leu Pro
385                     390                     395                     400
Leu Met His Thr Tyr Ala Gly Leu Ala Val Ile Cys Ala Leu Ile Gly
                 405                     410                     415
Phe Ser Ser Gly Tyr Phe Ser Leu Met Pro Val Val Thr Glu Asp Leu
             420                     425                     430
Val Gly Ile Glu His Leu Ala Asn Ala Tyr Gly Ile Ile Ile Cys Ala
             435                     440                     445
Asn Gly Ile Ser Ala Leu Leu Gly Pro Pro Phe Ala Gly Trp Ile Tyr
     450                     455                     460
Asp Ile Thr Gln Lys Tyr Asp Phe Ser Phe Tyr Ile Cys Gly Leu Leu
465                     470                     475                     480
Tyr Met Ile Gly Ile Leu Phe Leu Leu Ile Gln Pro Cys Ile Arg Ile
                 485                     490                     495
Ile Glu Gln Ser Arg Arg Lys Tyr Met Asp Gly Ala His Val
             500                     505                     510
```

<210> 3
<211> 1533
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (1)...(1533)

<400> 3
```
atg tat acc agt cat gaa gat att ggg tat gat ttt gaa gat ggc ccc      48
Met Tyr Thr Ser His Glu Asp Ile Gly Tyr Asp Phe Glu Asp Gly Pro
 1               5                   10                  15

aaa gac aaa aag aca ctg aag ccc cac cca aac att gat ggc gga tgg      96
Lys Asp Lys Lys Thr Leu Lys Pro His Pro Asn Ile Asp Gly Gly Trp
                20                  25                  30

gct tgg atg atg gtg ctc tcc tct ttc ttt gtg cac atc ctc atc atg     144
Ala Trp Met Met Val Leu Ser Ser Phe Phe Val His Ile Leu Ile Met
            35                  40                  45

ggc tcc cag atg gcc ctg ggt gtc ctc aac gtg gaa tgg ctg gaa gaa     192
Gly Ser Gln Met Ala Leu Gly Val Leu Asn Val Glu Trp Leu Glu Glu
```

```
ttc cac cag agc cgc ggc ctg acc gcc tgg gtc agc tcc ctc agc atg    240
Phe His Gln Ser Arg Gly Leu Thr Ala Trp Val Ser Ser Leu Ser Met
 65              70                  75                  80

ggc atc acc ttg ata gtg ggc cct ttc atc ggc ttg ttc att aac acc    288
Gly Ile Thr Leu Ile Val Gly Pro Phe Ile Gly Leu Phe Ile Asn Thr
                85                  90                  95

tgt ggg tgc cgc cag act gcg atc att gga ggg ctc gtc aac tcc ctg    336
Cys Gly Cys Arg Gln Thr Ala Ile Ile Gly Gly Leu Val Asn Ser Leu
            100                 105                 110

ggc tgg gtg ttg agt gcc tat gct gca aac gtg cat tat ctc ttc att    384
Gly Trp Val Leu Ser Ala Tyr Ala Ala Asn Val His Tyr Leu Phe Ile
            115                 120                 125

act ttt gga gtc gca gct ggc ctg ggc agc ggg atg gcc tac ctg cca    432
Thr Phe Gly Val Ala Ala Gly Leu Gly Ser Gly Met Ala Tyr Leu Pro
        130                 135                 140

gcg gtg gtc atg gtg ggc agg tat ttc cag aag aga cgc gcc ctc gcc    480
Ala Val Val Met Val Gly Arg Tyr Phe Gln Lys Arg Arg Ala Leu Ala
145                 150                 155                 160

cag ggc ctc agc acc acg ggg acc gga ttc ggt acg ttc cta atg act    528
Gln Gly Leu Ser Thr Thr Gly Thr Gly Phe Gly Thr Phe Leu Met Thr
                165                 170                 175

gtg ctg ctg aag tac ctg tgc gca gag tac ggc tgg agg aat gcc atg    576
Val Leu Leu Lys Tyr Leu Cys Ala Glu Tyr Gly Trp Arg Asn Ala Met
            180                 185                 190

ttg atc caa ggt gcc gtt tcc cta aac ctg tgt gtt tgt ggg gcg ctc    624
Leu Ile Gln Gly Ala Val Ser Leu Asn Leu Cys Val Cys Gly Ala Leu
            195                 200                 205

atg agg ccc ctc tct cct ggt aaa aac cca aac gac cca gga gag aaa    672
Met Arg Pro Leu Ser Pro Gly Lys Asn Pro Asn Asp Pro Gly Glu Lys
            210                 215                 220

gat gtg cgt ggc ctg cca gcg cac tcc aca gaa tct gtg aag tca act    720
Asp Val Arg Gly Leu Pro Ala His Ser Thr Glu Ser Val Lys Ser Thr
225                 230                 235                 240

gga cag cag gga aga aca gaa gag aag gat ggt ggg ctc ggg aac gag    768
Gly Gln Gln Gly Arg Thr Glu Glu Lys Asp Gly Gly Leu Gly Asn Glu
                245                 250                 255

gag acc ctc tgc gac ctg caa gcc cag gag tgc ccc gat cag gcc ggg    816
Glu Thr Leu Cys Asp Leu Gln Ala Gln Glu Cys Pro Asp Gln Ala Gly
            260                 265                 270

cac agg aag aac atg tgt gcc ctc cgg att ctg aag act gtc agc tgg    864
His Arg Lys Asn Met Cys Ala Leu Arg Ile Leu Lys Thr Val Ser Trp
            275                 280                 285

ctc acc atg aga gtc agg aag ggc ttc gag gac tgg tat tcg ggc tac    912
Leu Thr Met Arg Val Arg Lys Gly Phe Glu Asp Trp Tyr Ser Gly Tyr
        290                 295                 300
```

```
ttt ggg aca gcc tct cta ttt aca aat cga atg ttt gta gcc ttt att    960
Phe Gly Thr Ala Ser Leu Phe Thr Asn Arg Met Phe Val Ala Phe Ile
305             310             315             320

ttc tgg gct ttg ttt gca tac agc agc ttt gtc atc ccc ttc att cac    1008
Phe Trp Ala Leu Phe Ala Tyr Ser Ser Phe Val Ile Pro Phe Ile His
            325             330             335

ctc cca gaa atc gtc aat ttg tat aac tta tcg gag caa aac gac gtt    1056
Leu Pro Glu Ile Val Asn Leu Tyr Asn Leu Ser Glu Gln Asn Asp Val
            340             345             350

ttc cct ctg acg tca att ata gca ata gtt cac atc ttt gga aaa gtg    1104
Phe Pro Leu Thr Ser Ile Ile Ala Ile Val His Ile Phe Gly Lys Val
            355             360             365

atc ctg ggc gtc ata gcc gac ttg cct tgc att agt gtt tgg aat gtc    1152
Ile Leu Gly Val Ile Ala Asp Leu Pro Cys Ile Ser Val Trp Asn Val
            370             375             380

ttc ctg ttg gcc aac ttc acc ctt gtc ctc agt att ttt att ctg ccg    1200
Phe Leu Leu Ala Asn Phe Thr Leu Val Leu Ser Ile Phe Ile Leu Pro
385             390             395             400

ttg atg cac acg tac gct ggc ctg gcg gtc atc tgt gcg ctg ata ggg    1248
Leu Met His Thr Tyr Ala Gly Leu Ala Val Ile Cys Ala Leu Ile Gly
            405             410             415

ttt tcc agt ggt tat ttc tcc cta atg ccc gta gtg act gaa gac ttg    1296
Phe Ser Ser Gly Tyr Phe Ser Leu Met Pro Val Val Thr Glu Asp Leu
            420             425             430

gtt ggc att gaa cac ctg gcc aat gcc tac ggc atc atc atc tgt gct    1344
Val Gly Ile Glu His Leu Ala Asn Ala Tyr Gly Ile Ile Ile Cys Ala
            435             440             445

aat ggc atc tct gca ttg ctg gga cca cct ttt gca ggg tgg atc tat    1392
Asn Gly Ile Ser Ala Leu Leu Gly Pro Pro Phe Ala Gly Trp Ile Tyr
            450             455             460

gac atc acg caa aaa tat gat ttt tcc ttc tac ata tgt ggt ttg ctt    1440
Asp Ile Thr Gln Lys Tyr Asp Phe Ser Phe Tyr Ile Cys Gly Leu Leu
465             470             475             480

tac atg ata gga ata ctc ttt tta ctt att cag ccg tgc att cga att    1488
Tyr Met Ile Gly Ile Leu Phe Leu Leu Ile Gln Pro Cys Ile Arg Ile
            485             490             495

ata gaa caa tcc aga aga aaa tac atg gat ggt gca cat gtt tag    1533
Ile Glu Gln Ser Arg Arg Lys Tyr Met Asp Gly Ala His Val *
            500             505             510
```

<210> 4
<211> 611
<212> PRT
<213> Artificial Sequence

<220>

- 7 -

<223> consensus

<400> 4
Ser Phe Leu Ile Asn Gly Phe Thr Asp Gly Phe Pro Lys Ser Phe Gly
1   5   10   15
Leu Ile Phe Phe Arg Glu Leu Gln Glu Glu Phe Gln Ala Ser Asn Ser
            20   25   30
Glu Thr Ser Trp Asp Ser Ile Ser Ser Ile Leu Leu Ala Val Leu Leu
        35   40   45
Phe Ala Gly Pro Leu Ala Ser Ile Leu Val Asn Arg Phe Gly Cys Arg
    50   55   60
Leu Val Thr Ile Ala Gly Gly Leu Leu Ala Ser Ser Gly Met Val Leu
65   70   75   80
Ala Ser Phe Ala Thr Asn Ile Ser Glu Leu Tyr Leu Thr Phe Gly Val
            85   90   95
Ile Thr Gly Leu Gly Phe Ala Phe Ile Tyr Leu Pro Ala Ile Val Ile
            100   105   110
Ile Thr Ser Tyr Phe Glu Lys Lys Arg Ser Leu Ala Thr Gly Ile Ala
            115   120   125
Val Ala Gly Ser Gly Val Gly Thr Phe Val Leu Ala Pro Leu Asn Pro
    130   135   140
Asp Gln Phe Leu Ile Glu Asn Tyr Gly Ser Lys Trp Arg Gly Ala Leu
145   150   155   160
Leu Phe Phe Gly Gly Met Gly Tyr Val Ile Ala Ile Trp Ser Val Ala
            165   170   175
Ile Val Leu Asn Cys Cys Ile Ala Gly Ala Leu Phe Arg Pro Leu Pro
            180   185   190
Ser Glu Lys Val Lys Gln Thr Lys Leu Ala Lys Ala Glu Glu Pro Lys
            195   200   205
Glu Ala Leu Lys Ser Lys Glu Asn Glu Ala Ser Glu Ser Ile Asp Ser
    210   215   220
Ile Arg Ser Ala Ala Lys Ala Ile Val Ser Pro Glu Thr Pro Ala Leu
225   230   235   240
Ser Leu Ser Pro Glu Leu Thr Pro Lys Lys Asp Gln Leu Gln Lys Leu
            245   250   255
Leu Lys Thr Ser Arg Thr Arg Ser Ser Asn Gly Ala Lys Leu Leu Asp
            260   265   270
Phe Ser Val Leu Lys Asp Ala Arg Gly Phe Leu Leu Tyr Ala Ser Ser
            275   280   285
Gly Ser Leu Ala Ser Leu Gly Thr Gln Leu Phe Leu Pro Gly Ser Ile
    290   295   300
Phe Leu Val Asn Phe Ala Lys Ser Leu Gly Glu Ser Leu Ser Ser Val
305   310   315   320
Lys Ser Lys Glu Ala Ala Phe Leu Leu Ser Ile Leu Gly Asp Ser Ser
            325   330   335
Asp Lys Glu Gly Phe Gly Gly Ile Phe Ala Arg Pro Ala Thr Leu Leu
            340   345   350
Ser Phe Leu Gly Phe Val Ala Asn Leu Lys Glu Thr Lys Ser Asn Arg
            355   360   365
Pro Val Leu Ile Tyr Leu Leu Ser Leu Cys Ser Ile Val Ala Val Val
    370   375   380
Ile Asn Gly Ile Leu Ser Arg Leu Ala Ser Ala Leu Ala Gly Ser Arg
385   390   395   400
Lys Glu Lys Lys Ile Lys Ser Met Ile Asp Lys Ile Glu Leu Lys Ser
            405   410   415
Thr Phe Trp Gly Leu Phe Leu Phe Ser Leu Phe Phe Gly Val Gly Phe
            420   425   430
Gly Ser Lys Lys Ala Val Val Ile Leu Ala Leu Gly Phe Leu Leu Phe
            435   440   445
Ser Ile Leu Tyr Ala Ile Pro Val Val Gly Leu Gln Lys Tyr Ser Ser
    450   455   460

- 8 -

```
Ala Leu Gly Leu Thr Glu Thr Asp Ala Ser Thr Leu Ile Glu Ala Ile
465                 470                 475                 480
Ala Val Leu Asn Ile Ile Gly Arg Pro Leu Ala Gly Leu Leu Ala Asp
                485                 490                 495
Lys Thr Lys Asn Arg Lys Leu Ala Ile Tyr Asn Leu Ser Leu Ile Leu
            500                 505                 510
Cys Gly Leu Phe Val Ala Phe Ala Pro Leu Ala Thr Ile Phe Leu Gly
        515                 520                 525
Leu Ala Phe Tyr Cys Val Leu Phe Gly Ser Ile Val Phe Leu Leu Ala
    530                 535                 540
Tyr Ala Phe Lys Gly Phe Cys Lys Gly Ser Tyr Ile Ala Leu Thr Ser
545                 550                 555                 560
Val Ile Ala Val Asp Leu Thr Gly Leu Asp Lys Leu Ser Asn Ala Phe
                565                 570                 575
Gly Leu Leu Leu Leu Phe Gln Gly Val Ala Thr Leu Val Gly Pro Pro
            580                 585                 590
Ile Ala Gly Leu Leu Lys Asp Leu Thr Gly Ser Tyr Lys Val Ser Phe
            595                 600                 605
Tyr Phe Ala
    610


<210> 5
<211> 487
<212> PRT
<213> homo sapiens

<400> 5
Met Leu Lys Arg Glu Gly Lys Val Gln Pro Tyr Thr Lys Thr Leu Asp
  1                 5                  10                  15
Gly Gly Trp Gly Trp Met Ile Val Ile His Phe Phe Leu Val Asn Val
                20                  25                  30
Phe Val Met Gly Met Thr Lys Thr Phe Ala Ile Phe Phe Val Val Phe
        35                  40                  45
Gln Glu Glu Phe Glu Gly Thr Ser Glu Gln Ile Gly Trp Ile Gly Ser
    50                  55                  60
Ile Met Ser Ser Leu Arg Phe Cys Ala Gly Pro Leu Val Ala Ile Ile
65                  70                  75                  80
Cys Asp Ile Leu Gly Glu Lys Thr Thr Ser Ile Leu Gly Ala Phe Val
                85                  90                  95
Val Thr Gly Gly Tyr Leu Ile Ser Ser Trp Ala Thr Ser Ile Pro Phe
            100                 105                 110
Leu Cys Val Thr Met Gly Leu Leu Pro Gly Leu Gly Ser Ala Phe Leu
        115                 120                 125
Tyr Gln Val Ala Ala Val Val Thr Thr Lys Tyr Phe Lys Lys Arg Leu
    130                 135                 140
Ala Leu Ser Thr Ala Ile Ala Arg Ser Gly Met Gly Leu Thr Phe Leu
145                 150                 155                 160
Leu Ala Pro Phe Thr Lys Phe Leu Ile Asp Leu Tyr Asp Trp Thr Gly
                165                 170                 175
Ala Leu Ile Leu Phe Gly Ala Ile Ala Leu Asn Leu Val Pro Ser Ser
            180                 185                 190
Met Leu Leu Arg Pro Ile His Ile Lys Ser Glu Asn Asn Ser Gly Ile
        195                 200                 205
Lys Asp Lys Gly Ser Ser Leu Ser Ala His Gly Pro Glu Ala His Ala
    210                 215                 220
Thr Glu Thr His Cys His Glu Thr Glu Glu Ser Thr Ile Lys Asp Ser
225                 230                 235                 240
Thr Thr Gln Lys Ala Gly Leu Pro Ser Lys Asn Leu Thr Val Ser Gln
                245                 250                 255
Asn Gln Ser Glu Glu Phe Tyr Asn Gly Pro Asn Arg Asn Arg Leu Leu
```

- 9 -

```
                    260                      265                      270
Leu Lys Ser Asp Glu Glu Ser Asp Lys Val Ile Ser Trp Ser Cys Lys
         275                      280                      285
Gln Leu Phe Asp Ile Ser Leu Phe Arg Asn Pro Phe Phe Tyr Ile Phe
         290                      295                      300
Thr Trp Ser Phe Leu Leu Ser Gln Leu Ala Tyr Phe Ile Pro Thr Phe
305                      310                      315                      320
His Leu Val Ala Arg Ala Lys Thr Leu Gly Ile Asp Ile Met Asp Ala
                    325                      330                      335
Ser Tyr Leu Val Ser Val Ala Gly Ile Leu Glu Thr Val Ser Gln Ile
                    340                      345                      350
Ile Ser Gly Trp Val Ala Asp Gln Asn Trp Ile Lys Lys Tyr His Tyr
                    355                      360                      365
His Lys Ser Tyr Leu Ile Leu Cys Gly Ile Thr Asn Leu Leu Ala Pro
         370                      375                      380
Leu Ala Thr Thr Phe Pro Leu Leu Met Thr Tyr Thr Ile Cys Phe Ala
385                      390                      395                      400
Ile Phe Ala Gly Gly Tyr Leu Ala Leu Ile Leu Pro Val Leu Val Asp
                    405                      410                      415
Leu Cys Arg Asn Ser Thr Val Asn Arg Phe Leu Gly Leu Ala Ser Phe
         420                      425                      430
Phe Ala Gly Met Ala Val Leu Ser Gly Pro Pro Ile Ala Gly Trp Leu
         435                      440                      445
Tyr Asp Tyr Thr Gln Thr Tyr Asn Gly Ser Phe Tyr Phe Ser Gly Ile
         450                      455                      460
Cys Tyr Leu Leu Ser Ser Val Ser Phe Phe Phe Val Pro Leu Ala Glu
465                      470                      475                      480
Arg Trp Lys Asn Ser Leu Thr
                    485
```

```
<210> 6
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus

<221> VARIANT
<222> 1
<223> The amino acid at position 1 can be glu.

<221> VARIANT
<222> 3
<223> The amino acid at position 3 can be ser.

<221> VARIANT
<222> 4
<223> The amino acid at position 4 can be phe.

<221> VARIANT
<222> 5
<223> The amino acid at position 5 can be ala.

<400> 6
```

```
Asp Gly Gly Trp Gly Trp
 1               5
```

```
<210> 7
```

```
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus

<221> VARIANT
<222> 5
<223> The amino acid at position 5 can be lys.

<221> VARIANT
<222> 6
<223> The amino acid at position 6 can be leu.

<221> VARIANT
<222> 11
<223> The amino acid at position 11 can be ala.

<221> VARIANT
<222> (1)...(16)
<223> Xaa = Any Amino Acid

<400> 7
Tyr Phe Xaa Lys Arg Arg Xaa Leu Ala Xaa Gly Xaa Ala Xaa Ala Gly
 1               5                   10                  15


<210> 8
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus

<221> VARIANT
<222> (1)...(22)
<223> Xaa = any amino acid

<400> 8
Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa
 1               5                   10                  15
Xaa Xaa Xaa Xaa Xaa Leu
                20
```